

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Tang, Y. Tom
Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
Patterson, Chandra
Batra, Sajeev
Baughn, Mariah R.

(ii) TITLE OF THE INVENTION: RAS PROTEINS

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: Word Perfect 6.1/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/766,551
(B) FILING DATE: DECEMBER 12, 1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0168-1 CIP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

PF-0168-3 DIV

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KIDNNOT05
- (B) CLONE: 627565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met Asn Ile Leu Ala Pro Val Arg Arg Asp Arg Val Leu Ala Glu
5 10 15
Leu Pro Gln Cys Leu Arg Lys Glu Ala Ala Leu His Gly His Lys
20 25 30
Asp Phe His Pro Arg Val Thr Cys Ala Cys Gln Glu His Arg Thr
35 40 45
Gly Thr Val Gly Phe Lys Ile Ser Lys Val Ile Val Val Gly Asp
50 55 60
Leu Ser Val Gly Lys Thr Cys Leu Ile Asn Arg Phe Cys Lys Asp
65 70 75
Thr Phe Asp Lys Asn Tyr Lys Ala Thr Ile Gly Val Asp Phe Glu
80 85 90
Met Glu Arg Phe Glu Val Leu Gly Ile Pro Phe Ser Leu Gln Leu
95 100 105
Trp Asp Thr Ala Gly Gln Glu Arg Phe Lys Cys Ile Ala Ser Thr
110 115 120
Tyr Tyr Arg Gly Ala Gln Ala Ile Ile Ile Val Phe Asn Leu Asn
125 130 135
Asp Val Ala Ser Leu Glu His Thr Lys Gln Trp Leu Ala Asp Ala
140 145 150
Leu Lys Glu Asn Asp Pro Ser Ser Val Leu Leu Phe Leu Val Gly
155 160 165
Ser Lys Lys Asp Leu Ser Thr Pro Ala Gln Tyr Ala Leu Met Glu
170 175 180
Lys Asp Ala Leu Gln Val Ala Gln Glu Met Lys Ala Glu Tyr Trp
185 190 195
Ala Val Ser Ser Leu Thr Gly Glu Asn Val Arg Glu Phe Phe Phe
200 205 210
Arg Val Ala Ala Leu Thr Phe Glu Ala Asn Val Leu Ala Glu Leu
215 220 225
Glu Lys Ser Gly Ala Arg Arg Ile Gly Asp Val Val Arg Ile Asn
230 235 240
Ser Asp Asp Ser Asn Leu Tyr Leu Thr Ala Ser Lys Lys Lys Pro
245 250 255
Thr Cys Cys Pro

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids

PF-0168-3 DIV

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: COLNNOT05
(B) CLONE: 775601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Gly	Ile	Leu	Phe	Thr	Arg	Ile	Trp	Arg	Leu	Phe	Asn	His	Gln	
			5						10					15	
Gly	Pro	Arg	Gly	Ser	Ser	Gln	Thr	Asn	Ala	Ala	Ala	Met	Ser	Ala	
			20						25					30	
Ser	Leu	Glu	His	Lys	Val	Ile	Ile	Val	Gly	Leu	Asp	Asn	Ala	Gly	
			35						40					45	
Lys	Thr	Thr	Ile	Leu	Tyr	Gln	Phe	Ser	Met	Asn	Glu	Val	Val	His	
			50						55					60	
Thr	Ser	Pro	Thr	Ile	Gly	Gly	Asn	Val	Glu	Glu	Ile	Ala	Ile	Asn	
			65						70					75	
Asn	Thr	Arg	Phe	Leu	Met	Trp	Asp	Ile	Gly	Gly	Gln	Glu	Ser	Leu	
			80						85					90	
Arg	Ser	Ser	Trp	Asn	Thr	Tyr	Tyr	Thr	Asn	Thr	Glu	Phe	Val	Ile	
			95						100					105	
Val	Val	Val	Asp	Ser	Thr	Asp	Arg	Glu	Arg	Ile	Ser	Val	Thr	Arg	
			110						115					120	
Glu	Glu	Leu	Tyr	Lys	Met	Leu	Ala	His	Glu	Asp	Pro	Arg	Lys	Ala	
			125						130					135	
Gly	Leu	Leu	Ile	Phe	Ala	Asn	Lys	Gln	Asp	Val	Lys	Glu	Cys	Met	
			140						145					150	
Thr	Val	Ala	Glu	Ile	Ser	Gln	Phe	Leu	Lys	Leu	Thr	Ser	Ile	Lys	
			155						160					165	
Asp	His	Gln	Trp	His	Ile	Gln	Ala	Cys	Cys	Ala	Leu	Thr	Gly	Glu	
			170						175					180	
Gly	Leu	Cys	Gln	Gly	Leu	Glu	Trp	Met	Met	Ser	Arg	Leu	Lys	Ile	
			185						190					195	
Arg															

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: UCMCL5T01
(B) CLONE: 1528559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

PF-0168-3 DIV

Met	Leu	Leu	Gly	Asp	Thr	Gly	Val	Gly	Lys	Thr	Cys	Phe	Leu	Ile	5	10	15
Gln	Phe	Lys	Asp	Gly	Ala	Phe	Leu	Ser	Gly	Thr	Phe	Ile	Ala	Thr	20	25	30
Val	Gly	Ile	Asp	Phe	Arg	Asn	Lys	Val	Val	Thr	Val	Asp	Gly	Val	35	40	45
Arg	Val	Lys	Leu	Gln	Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	50	55	60
Arg	Ser	Val	Thr	His	Ala	Tyr	Tyr	Arg	Asp	Ala	Gln	Ala	Leu	Leu	65	70	75
Leu	Leu	Tyr	Asp	Ile	Thr	Asn	Lys	Ser	Ser	Phe	Asp	Asn	Ile	Arg	80	85	90
Ala	Trp	Leu	Thr	Glu	Ile	His	Glu	Tyr	Ala	Gln	Arg	Asp	Val	Val	95	100	105
Ile	Met	Leu	Leu	Gly	Asn	Lys	Ala	Asp	Met	Ser	Ser	Glu	Arg	Val	110	115	120
Ile	Arg	Ser	Glu	Asp	Gly	Glu	Thr	Leu	Ala	Arg	Glu	Tyr	Gly	Val	125	130	135
Pro	Phe	Leu	Glu	Thr	Ser	Ala	Lys	Thr	Gly	Met	Asn	Val	Glu	Leu	140	145	150
Ala	Phe	Leu	Ala	Ile	Ala	Lys	Glu	Leu	Lys	Tyr	Arg	Ala	Gly	His	155	160	165
Gln	Ala	Asp	Glu	Pro	Ser	Phe	Gln	Ile	Arg	Asp	Tyr	Val	Glu	Ser	170	175	180
Gln	Lys	Lys	Arg	Ser	Ser	Cys	Cys	Ser	Phe	Met					185	190	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT08
- (B) CLONE: 1651593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

Met	Asn	Ile	Leu	Ala	Pro	Val	Arg	Arg	Asp	Arg	Val	Leu	Ala	Glu	5	10	15
Leu	Pro	Gln	Cys	Leu	Arg	Lys	Glu	Ala	Ala	Leu	His	Gly	His	Lys	20	25	30
Asp	Phe	His	Pro	Arg	Val	Thr	Cys	Ala	Cys	Gln	Glu	His	Arg	Thr	35	40	45
Gly	Thr	Val	Gly	Arg	Phe	Lys	Ile	Ser	Lys	Val	Ile	Val	Val	Gly	50	55	60
Asp	Leu	Ser	Val	Gly	Lys	Thr	Cys	Leu	Ile	Asn	Arg	Phe	Cys	Lys	65	70	75

PF-0168-3 DIV

Asp	Thr	Phe	Asp	Lys	Asn	Tyr	Lys	Ala	Thr	Ile	Gly	Val	Asp	Phe	
				80					85					90	
Glu	Met	Glu	Arg	Phe	Glu	Val	Leu	Gly	Ile	Pro	Phe	Ser	Leu	Gln	
				95					100					105	
Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Lys	Cys	Ile	Ala	Ser	
				110					115					120	
Thr	Tyr	Tyr	Arg	Gly	Ala	Gln	Ala	Ile	Ile	Ile	Val	Phe	Asn	Leu	
				125					130					135	
Asn	Asp	Val	Ala	Ser	Leu	Glu	His	Thr	Lys	Gln	Trp	Leu	Ala	Asp	
				140					145					150	
Ala	Leu	Lys	Glu	Asn	Asp	Pro	Ser	Ser	Val	Leu	Leu	Phe	Leu	Val	
				155					160					165	
Gly	Ser	Lys	Lys	Asp	Leu	Ser	Thr	Pro	Ala	Gln	Tyr	Ala	Leu	Met	
				170					175					180	
Glu	Lys	Asp	Ala	Leu	Gln	Val	Ala	Gln	Glu	Met	Lys	Ala	Glu	Tyr	
				185					190					195	
Trp	Ala	Val	Ser	Ser	Leu	Thr	Gly	Glu	Asn	Val	Arg	Glu	Phe	Phe	
				200					205					210	
Phe	Arg	Val	Ala	Ala	Leu	Thr	Phe	Glu	Ala	Asn	Val	Leu	Ala	Glu	
				215					220					225	
Leu	Glu	Lys	Ser	Gly	Ala	Arg	Arg	Ile	Gly	Asp	Val	Val	Arg	Ile	
				230					235					240	
Asn	Ser	Asp	Asp	Ser	Asn	Leu	Tyr	Leu	Thr	Ala	Ser	Lys	Lys	Lys	
				245					250					255	
Pro	Thr	Cys	Cys	Pro											
				260											

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT05
- (B) CLONE: 1673056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Leu	Pro	Ile	Phe	Ile	Ser	Asn	Trp	Trp	Leu	Asp	Met	Leu	Gly	
				5					10					15	
Leu	Val	Trp	Glu	Pro	Ser	Asp	Lys	Leu	Lys	Gly	Trp	Ile	Arg	Lys	
				20					25					30	
Arg	Leu	Thr	Thr	Pro	Leu	Val	Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	
				35					40					45	
Leu	Arg	Thr	Leu	Ser	Tyr	Pro	Gln	Thr	Val	Gly	Glu	Thr	Tyr	Gly	
				50					55					60	
Lys	Asp	Ile	Thr	Ser	Arg	Gly	Lys	Asp	Met	Pro	Ile	Ala	Asp	Val	
				65					70					75	

PF-0168-3 DIV

Phe	Leu	Ile	Cys	Phe	Ser	Leu	Val	Ser	Pro	Ala	Ser	Phe	Glu	Asn	
				80					85					90	
Val	Arg	Ala	Lys	Trp	Tyr	Pro	Glu	Val	Arg	His	His	Cys	Pro	Asn	
				95					100					105	
Thr	Pro	Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	
				110					115					120	
Lys	Asp	Thr	Ile	Glu	Lys	Leu	Lys	Glu	Lys	Lys	Leu	Thr	Pro	Ile	
				125					130					135	
Thr	Tyr	Pro	Gln	Gly	Leu	Ala	Met	Ala	Lys	Glu	Ile	Gly	Ala	Val	
				140					145					150	
Lys	Tyr	Leu	Glu	Cys	Ser	Ala	Leu	Thr	Gln	Arg	Gly	Leu	Lys	Thr	
				155					160					165	
Val	Phe	Asp	Glu	Ala	Ile	Arg	Ala	Val	Ile	Cys	Pro	Pro	Pro	Val	
				170					175					180	
Lys	Lys	Arg	Lys	Arg	Lys	Cys	Leu	Met	Leu						
				185					190						

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT10
- (B) CLONE: 2703745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Thr	Thr	Leu	Asn	Leu	Leu	Ala	His	Arg	Arg	Leu	Thr	Arg	Leu	
				5					10					15	
Tyr	Leu	Leu	Gly	Thr	Leu	Gln	Trp	Gly	Ser	Leu	Val	Ser	Ser	Trp	
				20					25					30	
Arg	Leu	Cys	Lys	Asn	Glu	Phe	Arg	Glu	Asn	Ile	Ser	Ala	Thr	Leu	
				35					40					45	
Gly	Val	Asp	Phe	Gln	Met	Lys	Thr	Leu	Ile	Val	Asp	Gly	Glu	Arg	
				50					55					60	
Thr	Val	Leu	Gln	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	
				65					70					75	
Ser	Ile	Ala	Lys	Ser	Tyr	Phe	Arg	Lys	Ala	Asp	Gly	Val	Leu	Leu	
				80					85					90	
Leu	Tyr	Asp	Val	Thr	Cys	Glu	Lys	Ser	Phe	Leu	Asn	Ile	Arg	Glu	
				95					100					105	
Trp	Val	Asp	Met	Ile	Glu	Asp	Ala	Ala	His	Glu	Thr	Val	Pro	Ile	
				110					115					120	
Met	Leu	Val	Gly	Asn	Lys	Ala	Asp	Ile	Arg	Asp	Thr	Ala	Ala	Thr	
				125					130					135	
Glu	Gly	Gln	Lys	Cys	Val	Pro	Gly	His	Phe	Gly	Glu	Lys	Leu	Ala	
				140					145					150	

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PF-0168-3 DIV

Met	Thr	Tyr	Gly	Ala	Leu	Phe	Cys	Glu	Thr	Ser	Ala	Lys	Asp	Gly	
				155					160					165	
Ser	Asn	Ile	Val	Glu	Ala	Val	Leu	His	Leu	Ala	Arg	Glu	Val	Lys	
				170					175					180	
Lys	Arg	Thr	Asp	Lys	Asp	Asp	Ser	Arg	Ser	Ile	Thr	Asn	Leu	Thr	
				185					190					195	
Gly	Thr	Asn	Ser	Lys	Lys	Ser	Pro	Gln	Met	Lys	Asn	Cys	Cys	Asn	
				200					205					210	
Gly															

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENCNOT06
- (B) CLONE: 3440519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Ser	Ser	Val	Phe	Gly	Lys	Pro	Arg	Ala	Gly	Ser	Gly	Pro	Gln	
				5					10					15	
Ser	Ala	Pro	Leu	Glu	Val	Asn	Leu	Ala	Ile	Leu	Gly	Arg	Arg	Gly	
				20					25					30	
Ala	Gly	Lys	Ser	Ala	Leu	Thr	Val	Lys	Phe	Leu	Thr	Lys	Arg	Phe	
				35					40					45	
Ile	Ser	Glu	Tyr	Asp	Pro	Asn	Leu	Glu	Asp	Thr	Tyr	Ser	Ser	Glu	
				50					55					60	
Glu	Thr	Val	Asp	His	Gln	Pro	Val	His	Leu	Arg	Val	Met	Asp	Thr	
				65					70					75	
Ala	Asp	Leu	Asp	Thr	Pro	Arg	Asn	Cys	Glu	Arg	Tyr	Leu	Asn	Trp	
				80					85					90	
Ala	His	Ala	Phe	Leu	Val	Val	Tyr	Ser	Val	Asp	Ser	Arg	Gln	Ser	
				95					100					105	
Phe	Asp	Ser	Ser	Ser	Ser	Tyr	Leu	Glu	Leu	Leu	Ala	Leu	His	Ala	
				110					115					120	
Lys	Glu	Thr	Gln	Arg	Ser	Ile	Pro	Ala	Leu	Leu	Leu	Gly	Asn	Lys	
				125					130					135	
Leu	Asp	Met	Ala	Gln	Tyr	Arg	Gln	Val	Thr	Lys	Ala	Glu	Gly	Val	
				140					145					150	
Ala	Leu	Ala	Gly	Arg	Phe	Gly	Cys	Leu	Phe	Phe	Glu	Val	Ser	Ala	
				155					160					165	
Cys	Leu	Asp	Phe	Glu	His	Val	Gln	His	Val	Phe	His	Glu	Ala	Val	
				170					175					180	
Arg	Glu	Ala	Arg	Arg	Glu	Leu	Glu	Lys	Ser	Pro	Leu	Thr	Arg	Pro	
				185					190					195	
Leu	Phe	Ile	Ser	Glu	Glu	Arg	Ala	Leu	Pro	His	Gln	Ala	Pro	Leu	

PF-0168-3 DIV

	200		205		210
Thr Ala Arg His Gly Leu Ala Ser Cys Thr Phe Asn Thr Leu Ser					
	215		220		225
Thr Ile Asn Leu Lys Glu Met Pro Thr Val Ala Gln Ala Lys Leu					
	230		235		240
Val Thr Val Lys Ser Ser Arg Ala Gln Ser Lys Arg Lys Ala Pro					
	245		250		255
Thr Leu Thr Leu Leu Lys Gly Phe Lys Ile Phe					
	260		265		

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KIDNNOT05
- (B) CLONE: 627565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

GGCGCCCTGC	AAGGCCGCAG	GCAGGATGAA	CATTCTGGCA	CCCGTGCGGA	GGGATCGCGT	60
CCTGGCGGAG	CTGCCCCAGT	GCCTGAGGAA	GGAGGCCGCT	TTGCACGGGC	ACAAAGACTT	120
CCACCCCCCG	GTCACCTGCG	CCTGCCAGGA	GCACCGGACA	GGCACCCTGG	GATTTAAGAT	180
CTCCAAGGTC	ATTGTGGTGG	GGGACCTGTC	GGTGGGGAAG	ACTTGCCTCA	TTAATAGGTT	240
CTGCAAAGAC	ACCTTTGATA	AGAATTACAA	GGCCACCATT	GGAGTGGACT	TCGAGATGGA	300
ACGATTTGAG	GTGCTGGGCA	TTCCCTTCAG	TTTGCAGCTT	TGGGATACCG	CTGGGCAGGA	360
GAGGTTCAAA	TGCATTGCAT	CAACCTACTA	TAGAGGAGCT	CAAGCCATCA	TCATTGTCTT	420
CAACCTGAAT	GATGTGGCAT	CTCTGGAACA	TACCAAGCAG	TGGCTGGCCG	ATGCCCTGAA	480
GGAGAATGAC	CCTTCCAGTG	TGCTTCTCTT	CCTTGTAGGT	TCCAAGAAGG	ATCTGAGTAC	540
CCCTGCTCAG	TATGCGCTGA	TGGAGAAAGA	CGCCCTCCAG	GTGGCCCAGG	AGATGAAGGC	600
TGAGTACTGG	GCAGTCTCAT	CTCTCACTGG	TGAGAATGTC	CGAGAATTCT	TCTTCCGTGT	660
GGCAGCACTG	ACCTTTGAGG	CCAATGTGCT	GGCTGAGCTG	GAGAAATCGG	GGGCTCGACG	720
CATTGGGGAT	GTTGTCCGCA	TCAACAGTGA	TGACAGCAAC	CTCTACCTAA	CTGCCAGCAA	780
GAAGAAGCCC	ACATGTTGCC	CATGAGGGCT	GAGGAGACTG	TTCAGAGACT	GCCCAGCCCT	840
AGGGCACTGT	GCCACCCTCA	TTCTTCCAGA	GCTTGACCCC	TGGACATTTG	CACTGACTTT	900
ATCCAGACCA	AAGAGCTGCC	TCTTGGTGGC	AGTATTCCCA	CAGAGGGGTA	GCTGGGATCA	960
TGCTAGTCAC	TTCCTGCCCC	CAGGCACCGT	GCCAAAGACT	GGATGCCCCC	TACTCCTCAG	1020
GGGACTGTCC	AGGGCGCCCA	GTGGTAGTGA	GGGAGAGTGT	CTCTGTTCTT	TTGCTCAGCC	1080
TGCTGGGCCC	TTTGTGTTTG	AGGATGCTTA	ATGATTCCAG	CCTCTCACTG	TGCCTTATGC	1140
ATTAAAATTT	CTTTGTTACG	AGCAAAAAAA	AA			1172

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1469 base pairs
- (B) TYPE: nucleic acid

PF-0168-3 DIV

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: COLNNOT05
(B) CLONE: 775601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9 :

GAGCCAGGCG AGTGCCGCGG CGGAGCGCGG TGNCTTTGTC GCGCGGNANG GGGCCTGGGC 60
TTCGGCTCCC TCCGGTTCCC TGGAAGCGGG CCCNGACCAG NCGGAGCAGC AGCAGAGGCG 120
GAGNTCCAGC NGTCTCTCTC CTCCCCCTCA GCCTGAGCCG GGGGAANCAG NCGCCCGGGT 180
GTCTGGAGGG GGGGGGGTCC GCTGCCCGAG AATGGGAATT CTCTTCACTA GAATATGGAG 240
ACTGTTCAAT CACCAGGGCC CGCGAGGCTC GTCGCAGACG AACGCGGCGG CGATGTCCGC 300
GAGCCTAGAG CACAAAGTTA TCATTGTTGG GCTGGATAAT GCAGGAAAA CTACCATTCT 360
TTACCAATTT TCTATGAACG AAGTTGTACA TACATCTCCT ACAATAGGAG GTAATGTAGA 420
AGAGATAGCG ATTAATAATA CACGTTTCCT AATGTGGGAT ATTGGTGGCC AAGAATCTCT 480
TCGTTCTTCC TGAACACTT ACTATACTAA CACAGAGTTT GTAATAGTTG TTGTGGACAG 540
TACAGACAGA GAGAGGATTT CTGTAAC TAGAAGAACTC TATAAAATGT TAGCGCATGA 600
GGACCAAGA AAAGCTGGAT TGCTGATTTT TGCTAATAAA CAAGATGTTA AAGAATGCAT 660
GACTGTAGCA GAAATCTCCC AGTTTTTGAA GCTAACTTCT ATTAAAGATC ACCAGTGGCA 720
TATCCAGGCA TGCTGTGCTC TAACTGGCGA GGGATTGTGC CAAGGACTTG AATGGATGAT 780
GTCACGACTT AAGATTAGAT GATCTCTACT GACCTCTACT CATAGATTTT GTATAAATGA 840
AGTGCTGGAC TTTACCTGAA AGCTGCAAAA ATTAATGGTT TAGATATATT TATAATAAAC 900
TGATTTAAAC TTTTCTATA AGAAGAAAAA TTAAGACCAC TTATTTGAAA ACAAAGATGA 960
AGTCTCACCT TCCAGTTTGC TTTCTCATTA GTTTTTTCCA AAGTAAGTTA TTGAAGCTGT 1020
GATTGACATT TTTCTCATAA TGAATCCTCT CAGGACATTG TGTAGCCTAT GGTAAGTACA 1080
AAGGGAGAGG AAGACATTTT GAATTTTAAG AGCTTTATTA TCAGTTTAAC CCTCCCTAGT 1140
TGAATGTTAT TTTCTTCTTG TTCCATTAAAG TCAGAATACA AATCAGCACA GATATTCGAA 1200
TGTTTCCAAT ATTTTAAAT GTAATGTTAC TTATGAAAAG TATTTTGCTT AAGGTTGTGT 1260
GTGTATTGTG TATATACCTC AAGTCAAGT TAATGGCATT GATTTATGTT CCAGACAAAA 1320
ATAACACAAA TAATAATATC CTTCTGTATA ACCACAATGA GATAAGTATT GGCATTAGTG 1380
TTCAGTGCCA TTTTATACTT TCTCTGTGTG TTCTCTGTAT TGTACTAACC AACCTCCCAA 1440
ATCGCTGAGC TGCTTGTTTA AAAAAAAA 1469

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 875 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: UCMCL5T01
(B) CLONE: 1528559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10 :

CGGGCAGGCC AGGCGCCGTT GCCACCCGGG ATGGCGAGGC CCCCAGCGC TCCCCGCCCT 60
GCAGTCCGAG CTACGACCTC ACGGGCAAGG TGATGCTTCT GGGAGACACA GGCCTCGGCA 120
AAACATGTTT CCTGATCCAA TTCAAAGACG GGGCCTTCCT GTCCGGAACC TTCATAGCCA 180
CCGTCGGCAT AGACTTCAGG AACAAGGTGG TGAATGTGGA TGGCGTGAGA GTGAAGCTGC 240

PF-0168-3 DIV

AGATCTGGGA CACCGCTGGG CAGGAACGGT TCCGAAGCGT CACCCATGCT TATTACAGAG 300
ATGCTCAGGC CTTGCTTCTG CTGTATGACA TCACCAACAA ATCTTCTTTC GACAACATCA 360
GGGCCTGGCT CACTGAGATT CATGAGTATG CCCAGAGGGA CGTGGTGATC ATGCTGCTAG 420
GCAACAAGGC GGATATGAGC AGCGAAAGAG TGATCCGTTC CGAAGACGGA GAGACCTTGG 480
CCAGGGAGTA CGGTGTTCCC TTCCTGGAGA CCAGCGCCAA GACTGGCATG AATGTGGAGT 540
TAGCCTTTCT GCCCATCGCC AAGGAACTGA AATACCGGGC CGGGCATCAG GCGGATGAGC 600
CCAGCTTCCA GATCCGAGAC TATGTAGAGT CCCAGAAGAA GCGCTCCAGC TGCTGCTCCT 660
TCATGTGAAT CCCAGGGGGC AGAGAGGAGG CTCTGGAGGC ACACAGGATG CAGCCTTCCC 720
CCTCCCAGGC CTGGCTTATT CCAAGAGGCT GAGCCAATGG GGAGAAAGAT GGAGGACTCA 780
CTGCACAGCC GCTTCCTAGC AGGGAGCTAT ACTCCAATC CTACTTGAGT TCCTGCGGTC 840
TCCCCGCATC CACAGGGAGG GTAAAACACT TAGGG 875

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT08
- (B) CLONE: 1651593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

CTGGCATCGC CAGATGCTGC GCACAGTCTC CGATTCCCCA TCACCAATTC GGCTGGGGTC 60
TGCGCGGGCC CGGCCCCCAG CAGACGGGAC TCCCCGCCCC CAATTGGCGG CCGAAGAGTC 120
TCCTCGCCCC AGAGTCATCT TCGGGACGCC CAGGGCCCGG GTGATTTTGG GCTCGCCGCG 180
GCCCCGGGTG ATTGTTTCAT CTCCGTGGCC CGCGGTGGTC GTAGCGTCTC CGAGACCGCG 240
GACTCCCGTA GGTCCCCGTG GCCCCGAGTT GTAGTCGGGA CACCCCGGCC GCGGGTAGTC 300
GTCGGGTCTC CACGCGCCCC GGTCTGCTGAC GCGGATCCGG CCTCGGCGCC TTCTCAGGGC 360
GCCCTGCAAG GCCGCAGGCA GGATGAACAT TCTGGCACCC GTGCGGAGGG ATCGCGTCCT 420
GGCGGAGCTG CCCCAGTGCC TGAGGAAGGA GGCCGCTTTG CACGGGCACA AAGACTTCCA 480
CCCCCGCGTC ACCTGCGCCT GCCAGGAGCA CCGGACAGGC ACCGTGGGCA GATTTAAGAT 540
CTCCAAGGTC ATTGTGGTGG GGGACCTGTC GGTGGGGAAG ACTTGCCCTCA TTAATAGGTT 600
CTGCAAAGAC ACCTTTGATA AGAATTACAA GGCCACCATT GGAGTGGACT TCGAGATGGA 660
ACGATTTGAG GTGCTGGGCA TTCCCTTCAG TTTGCAGCTT TGGGATACCG CTGGGCAGGA 720
GAGGTTCAAA TGCATTGCAT CAACCTACTA TAGAGGAGCT CAAGCCATCA TCATTGTCTT 780
CAACCTGAAT GATGTGGCAT CTCTGGAACA TACCAAGCAG TGGCTGGCCG ATGCCCTGAA 840
GGAGAATGAC CTTCCAGTG TGCTTCTCTT CTTGTAGGT TCCAAGAAGG ATCTGAGTAC 900
CCCTGCTCAG TATGCGCTGA TGGAGAAAGA CGCCCTCCAG GTGGCCAGG AGATGAAGGC 960
TGAGTACTGG GCAGTCTCAT CTCTCACTGG TGAGAATGTC CGAGAATTCT TCTTCCGTGT 1020
GGCAGCACTG ACCTTTGAGG CCAATGTGCT GGCTGAGCTG GAGAAATCGG GGGCTCGACG 1080
CATTGGGGAT GTTGTCCGCA TCAACAGTGA TGACAGCAAC CTCTACCTAA CTGCCAGCAA 1140
GAAGAAGCCC ACATGTTGCC CATGAGGGCT GAGGAGACTG TTCAGAGACT GCCCAGCCCT 1200
AGGGCACTGT GCCACCCTCA TTCCTCCAGA GCTTGACCCC TGGACATTTG CACTGACTTT 1260
ATCCAGACCA AAGAGCTGCC TCTTGGTGGC AGTATTCCCA CAGAGGGGTA GCTGGGATCA 1320
TGCTAGTCAC TTCTGCCCC CAGGCACCGT GCCAAAGACT GGATGCCCC TACTCCTCAG 1380
GGGACTGTCC AGGGCGCCCC GTGGTAGTGA GGGAGAGTGT CTCTGTTCTT TTGCTCAGCC 1440
TGCTGGGCC TTTGTGTTTG AGGATGCTTA ATGATCCAG CCTCTCACTG TGCCTTATGC 1500
ATTAATAATT CTTTGTTACG AGCAAAAAA AAA 1533

PF-0168-3 DIV

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT05
- (B) CLONE: 1673056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12 :

ATATTTTAGA AATCTAGCAT TTTAGAATTC TTGGGCATTT TTAAATACAG GTGAATATTT 60
GAATTTGGTT TGACACAAAA TACAGAATGG ATGAAGCATG CAGATGTTTG GCGTGTGCCC 120
CGAAGCACCC TCTACTCTGT CCTCTGCACC CACCCTTTGC GCCTCTGCGT CAGCCACAGC 180
TGCCCCGGA GCGAGTTCTC CTGAGGCCCT GGCTGTGCTG ACTCTAGGGC AGCGTGAGGG 240
TGGTTGTCAG CTGTGAAGGT GCCACTTACA CACTAAGTCC TCCTTCCTTG TGGAGGGAAG 300
GGCTCAAGTA GCAAATATTG GAGCCCCCGC TTGGTGCTGG GAGCTGTGAC AGGCAGCTCC 360
TGAAGAAGCA GTTTAATTGG AACCAGTGAC CATCTAAAAC TGTGTGTACT CTAAACCAGA 420
TTTTACAGAA ATATTGGAAT CATACCTTTA TACTTGATTT TTTCAATTTA GATAGTTAGG 480
CGTAAAGGAA GCCTCCTGAG GGTCTGGTCT GATCCTCCTG ATCCTTGAAG AGCTTCCAGC 540
ATCATTCTCC CTTCATGCTC CCCATTTTCA TAAGTAACTG GTGGCTTGAC ATGCTGGGTT 600
TGGTTTGGGA GCCCTCTGAC AAAGTGAAAG GGTGGATCAG GAAGCGTCTG ACCACACCAC 660
TGGTAGCTGG ACAAGAAGAT TATGACAGAT TACGCACCCT ATCCTATCCG CAAACAGTTG 720
GAGAAACGTA CGGTAAGGAT ATAACCTCCC GGGGCAAAGA CATGCCGATT GCCGATGTGT 780
TCTTAATTTG CTTTTCCCTT GTGAGTCTTG CATCATTTGA AAATGTCCGT GCAAAGTGGT 840
ATCCTGAGGT GCGGCACCAC TGTCCCAACA CTCCCATCAT CCTAGTGGGA ACTAAACTTG 900
ATCTTAGGGA TGATAAAGAC ACGATCGAGA AACTGAAGGA GAAGAAGCTG ACTCCCATCA 960
CCTATCCGCA GGGTCTAGCC ATGGCTAAGG AGATTGGTGC TGTAATAATAC CTGGAGTGCT 1020
CGGCGCTCAC ACAGCGAGGC CTCAAGACAG TGTGTGACGA AGCGATCCGA GCAGTCATCT 1080
GCCCCCTCC CGTGAAGAAG AGGAAGAGAA AATGCCTGAT GTTGTAATG TCTCAGCCCC 1140
TCGTCTTGT CCTGCCCTTG GACCTTTTGC GTC 1173

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT10
- (B) CLONE: 2703745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13 :

CAGCACTCTC GCCCCAGACA GACCTGGTAG ATGACAACGC TAAATCTTTT AGCTCACAGA 60
AGGCTTACAA GATTGTACTT GCTGGGGACG CTGCAGTGGG GAAGTCTAGT TTCCTCATGG 120
AGACTTTGCA AGAATGAATT TCGAGAAAAT ATAAGCGCCA CCTGGGAGT TGATTTCCAA 180
ATGAAAACCC TCATTGTGGA TGGAGAACGA ACAGTTCTGC AGCTCTGGGA TACAGCTGGT 240

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CAGGAGAGAT TCAGAAGTAT TGCCAAGTCT TACTTCAGAA AGGCAGATGG TGTTTTGCTG 300
CTGTATGATG TTACATGTGA GAAAAGCTTT CTTAACATAC GAGAATGGGT AGATATGATT 360
GAGGATGCAG CCCATGAGAC TGTTCCCATT ATGCTGGTAG GAAACAAGGC TGACATTCGT 420
GACACTGCTG CTACAGAGGG AAAAAAATGT GTCCCAGGGC ACTTTGGAGA GAAACTGGCC 480
ATGACGTATG GGGCATTATT CTGTGAAACA AGTGCCAAAG ATGGTTCTAA CATAGTGGAG 540
GCTGTTCTGC ACCTTGCTCG AGAAGTGAAA AAGAGAACTG ACAAGGATGA CAGCAGATCC 600
ATTACCAATC TAACCGGGAC CAATTCCAAA AAGTCACCAC AGATGAAGAA TTGTTGCAAT 660
GGCTAAATCC CAAACATCCT TGGCCTGTGA AGTCTTCATT TCCAGAATAC TGAATTTGTG 720
TGACTTATTT GGCTCTTAAC AGAGTGGCAC ATCCTACTGA CACTGTCCTA TGGAGAGTTA 780
CAGTGCAGGA AACCTGAACC CAG 803

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENCNOT06
- (B) CLONE: 3440519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14 :

GTCGCCATGT CCTCGGTGTT TGGAAAACCC CGCGCGGGCA GCGGGCCTCA GAGCGCGCCC 60
CTCGAGGTCA ACCTGGCCAT CCTGGGGCGC CGCGGGGCTG GCAAGTCTGC CCTGACCGTG 120
AAGTTTCTGA CCAAGAGGTT TATCAGTGAA TATGACCCCA ACTTGGAGGA CACCTACAGC 180
TCCGAGGAGA CTGTGGACCA CCAGCCTGTC CACCTGAGGG TCATGGACAC TGCAGACCTG 240
GACACCCCCA GGAAGTGGCA GCGCTACCTG AACTGGGCCC ATGCCTTCCT GGTGGTGTAC 300
AGCGTCGACA GCCGCCAGAG CTTTGATAGC AGCAGCAGCT ACCTGGAGCT GCTTGCCCTG 360
CACGCGAAGG AGACACAGCG CAGCATCCCT GCCCTGCTGC TGGGCAACAA GCTGGACATG 420
GCTCAGTACA GGCAAGTCAC CAAGGCAGAG GGTGTGGCTT TGGCAGGCAG GTTTGGGTGC 480
CTGTTTTTCG AGGTCTCTGC CTGTCTGGAC TTTGAGCACG TGCAGCATGT CTTCCACGAG 540
GCAGTGCGAG AGGCACGGCG GGAGCTGGAG AAGAGCCCCC TGACCCGGCC CCTCTTCATC 600
TCCGAGGAGA GGGCCCTGCC CCACCAGGCC CCGCTCACTG CGCGGCATGG GCTGGCCAGC 660
TGCACCTTCA ACACGCTCTC CACCATCAAC CTGAAGGAGA TGCCCACTGT GGCCCAAGGCC 720
AAGCTGGTCA CCGTGAAGTC ATCCCGGGCC CAGAGCAAGC GCAAGGCGCC TACCCTGACT 780
CTCCTGAAGG GCTTCAAGAT CTTCTGAGGC CCCCTCCCCA GGAAGCCTAG GCTCGGTGGC 840
TGGACAGGAC TGCAGCAGGA CAGGACTGG CTTCTCACCA CCAGCCTTTC 890